

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 23:44:32 ; Search time 1168.39 Seconds  
(without alignments)  
471.288 Million cell updates/sec

Title: US-09-913-524-32  
Perfect score: 34  
Sequence: 1 aggcctcgagggaaccggctgccatgcccaact 34

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estinu:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	251	14	T29423 EST79588 Hu
2	34	100.0	364	10	AW951334 EST363404
3	34	100.0	501	9	AI128256 qc33h05.x
4	34	100.0	884	13	BI520936 603071335
5	34	100.0	899	9	AL568487 AL568487
6	34	100.0	924	9	AL540575 AL540575

c	7	32.4	95.3	599	9	AI220927	AI220927 qg08a11.x
c	8	30	88.2	548	14	BQ013783	BQ013783 UI-1-BC1p
c	9	27.6	81.2	510	9	AI885743	AI885743 w161a07.x
	10	26	76.5	399	12	BE758121	BE758121 212839 MA
	11	26	76.5	464	13	BI849730	BI849730 477654 MA
	12	26	76.5	466	9	AA234854	AA234854 zr77q01.r
	13	26	76.5	561	12	BE721322	BE721322 188456 MA
	14	26	76.5	1074	13	BM460913	BM460913 AGENCOURT
	15	26	76.5	1118	13	BM461343	BM461343 AGENCOURT
c	16	25	73.5	641	13	BI186150	BI186150 UNL-P-FN-
	17	24.4	71.8	640	12	BG872889	BG872889 602794024
c	18	24.4	71.8	659	13	BI183158	BI183158 UNL-P-FN-
c	19	24.4	71.8	705	13	BI182159	BI182159 UNL-P-FN-
c	20	24.4	71.8	1172	13	BM461317	BM461317 AGENCOURT
c	21	23.4	68.8	613	10	AW55078	AW55078 L0249F11-
c	22	23.4	68.8	649	13	BI181741	BI181741 UNL-P-FN-
c	23	23.4	68.8	978	14	BM804780	BM804780 AGENCOURT
c	24	23	67.6	629	13	BM665951	BM665951 UI-E-DX1-
c	25	22.8	67.1	1129	13	BM461356	BM461356 AGENCOURT
c	26	22	64.7	582	14	C87829	C87829 C87829 Mous
c	27	21.4	62.9	669	17	AG148285	AG148285 Pan trogl
c	28	21.4	62.9	1521	13	BM563318	BM563318 AGENCOURT
c	29	21.2	62.4	466	10	AW475765	AW475765 un71h04.y
c	30	21.2	62.4	1009	17	CMS02E39	AL193230 Tetradon
c	31	21	61.8	252	13	BM135954	BM135954 WHE2603.F
c	32	21	61.8	384	9	AA219283	AA219283 zq17a11.s
c	33	21	61.8	604	12	BG042907	BG042907 sv28e10.y
c	34	20.8	61.2	227	9	AA030977	AA030977 mi46d09.r
c	35	20.8	61.2	488	9	AA979198	AA979198 LD33504.5
c	36	20.8	61.2	538	10	BB769745	BB769745 BB769745
c	37	20.8	61.2	542	9	AI515111	AI515111 LD46806.5
c	38	20.8	61.2	597	9	AI512705	AI512705 LD4660.5
c	39	20.8	61.2	787	12	BG199330	BG199330 RST18612
c	40	20.6	60.6	740	13	BI103224	BI103224 602899464
c	41	20.6	60.6	843	13	BI332823	BI332823 602985577
c	42	20.6	60.6	845	13	BI857862	BI857862 603388427
c	43	20.6	60.6	920	14	BQ962399	BQ962399 AGENCOURT
c	44	20.4	60.0	278	9	AV088622	AV088622 AV088622
c	45	20.4	60.0	343	13	BG961308	BG961308 PM2-CT026

## ALIGNMENTS

RESULT 1	T29423	EST79588 Human Placenta Homo sapiens cDNA similar to inhibin, alpha	251 bp	mRNA	linear	EST 06-SEP-1995
LOCUS	T29423	(HT:1847). mRNA sequence.				
DEFINITION	T29423					
ACCESSION	T29423					
VERSION	T29423.1	GI:611521				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	1 (bases 1 to 251)					
	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult					
	C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White					
	O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W., Clayton R.A.,					
	Cline R.T., Cotton M.D., Earle-Hughes J., Fine D.D., Fitzgerald					
	L.M., Fitzhugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A.,					
	Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr. P.S., Kelley J.M.,					
	Klimek K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M.,					
	Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M.,					
	Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R.,					
	Small A.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li F.,					
	Bednarek D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J.,					
	Dinke D., Feng P., Ferrie A., Fischer C., Hastings G.A., He W.-W.,					
	Hu J.-S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L.,					
	Kunsch C., Ji H., Li H., Meissner P.S., Olsen H., Raymond L., Wei					
	Y.-F., Wing J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Fannon					
	M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and					

Venter, J.C.  
Initial Assessment of Human Gene Diversity and Expression Patterns  
Based Upon 83 Million Basepairs of cDNA Sequence  
Nature 377, 3-174 (1995)  
96026280  
Contact: Venter, JC  
The Institute for Genomic Research  
932 Clopper Rd, Gaithersburg, MD 20878  
Tel: 3018699056  
Fax: 3018699423  
Email: tdbinfo@tdb.tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please contact the TIGR Database  
(tdbinfo@tdb.tigr.org)  
Seq primer: M13 Reverse.

FEATURES  
source  
1..251  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="ATCC (inhost):106213"  
/db\_xref="taxon:9606"  
/clone\_lib="Human Placenta"  
/note="Organ: placenta"  
47 a 85 c 67 g 51 t 1 others  
BASE COUNT  
ORIGIN

Query Match 100.0%; Score 34; DB 14; Length 251;  
Best Local Similarity 100.0%; Pred. No. 0.037;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGGAGACCGCTGCCATGCCAACT 34  
|||||  
DB 94 AGGCTCCGAGGAGACCGCTGCCATGCCAACT 127

RESULT 2  
AW951334  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 364)  
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt  
J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeaman, T.J. and  
Quackenbush, J.  
Assessment of gene expression patterns in a model of colon tumor  
metastasis using a 19,200 element cDNA microarray  
Unpublished (2000)  
Contact: John Quackenbush  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: johnq@tigr.org  
Plate: 26  
Seq primer: Reverse.

FEATURES  
source  
1..364  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="MAGE resequences, MAGE"  
/note="Vector: pBluescriptSKm"  
59 a 135 c 96 g 74 t  
BASE COUNT  
ORIGIN  
Query Match 100.0%; Score 34; DB 10; Length 364;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGGAGACCGCTGCCATGCCAACT 34  
|||||  
DB 94 AGGCTCCGAGGAGACCGCTGCCATGCCAACT 127

RESULT 3  
AW128256  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 501)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs.fda.gov  
This clone is available royalty-free through LILN; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 832 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 433.

FEATURES  
source  
1..501  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Soares\_pregnant\_uterus\_NBHPU"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pT73-Pac; Site: 1; Not I;  
Site: 2; Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5',  
ACTCGAGAGATCGCGCGCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by M. Fatima Ronaldo."

BASE COUNT 118 a 117 c 177 g 89 t  
ORIGIN  
Query Match 100.0%; Score 34; DB 9; Length 501;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGGAGACCGCTGCCATGCCAACT 34  
|||||  
DB 445 AGGCTCCGAGGAGACCGCTGCCATGCCAACT 412

RESULT 4  
B1520936  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 884)

FEATURES  
source  
1..884  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5163273 3",  
mRNA sequence.  
B1520936.1 GI:15345728  
EST.  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 884)

BASE COUNT 118 a 117 c 177 g 89 t  
ORIGIN  
Query Match 100.0%; Score 34; DB 9; Length 501;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGGAGACCGCTGCCATGCCAACT 34  
|||||  
DB 445 AGGCTCCGAGGAGACCGCTGCCATGCCAACT 412

RESULT 4  
B1520936  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 884)

# AUTHORS TITLE JOURNAL COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cdapts@mail.nih.gov](mailto:cdapts@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L14M1405 row: f column: 10  
High quality sequence start: 2  
High quality sequence stop: 726.  
Location/Qualifiers

## FEATURES

source

1..884  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5163273"  
/clone\_lib="NIH\_MGC\_119"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site: 2: EcoRV (destroyed); RNA source: normal medulla from  
anonymously male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

BASE COUNT 175 a 241 c 327 g 151 t

Query Match 100.0%; Score 34; DB 13; Length 884;  
Best Local Similarity 100.0%; Pred. No. 0.048;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGAACCGGCTGCCCATGCCCACT 34  
|||||  
DB 458 AGGCTCCGGAGAACCGGCTGCCCATGCCCACT 425

## RESULT 5

AL568487/c

LOCUS

DEFINITION AL568487 LTL1\_FLO02\_PL1 Homo sapiens cDNA clone CS0DE002YE07 3 prime  
mRNA sequence.

ACCESSION AL568487.1 GI:12922875

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 899)

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

Location/Qualifiers

1..899

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DE002YE07"

/clone\_lib="LTL1\_FLO02\_PL1"

/lab\_host="DH10B"

/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand

cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-stranded cDNA was digested with Not I

and cloned into the Not I and Eco RV sites of the

PCMVSPORT 6 vector. Library was constructed by Life

Technologies. Contact : Feng Liang Life Technologies, a

division of Invitrogen 9800 Medical Center Drive Rockville

, Maryland 20850, USA Fax : (1) 301 610 8371 Email :

[fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com>

end enriched, double-stranded cDNA was digested with Not I  
and cloned into the Not I and Eco RV sites of the  
PCMVSPORT 6 vector. Library was constructed by Life  
Technologies. Contact : Feng Liang Life Technologies, a  
division of Invitrogen 9800 Medical Center Drive Rockville  
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :  
[fliang@lifetech.com](mailto:fliang@lifetech.com) URL :  
<http://fulllength.invitrogen.com>

BASE COUNT 184 a 229 c 318 g 159 t 9 others

ORIGIN

Query Match 100.0%; Score 34; DB 9; Length 899;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGAACCGGCTGCCCATGCCCACT 34  
|||||  
DB 458 AGGCTCCGGAGAACCGGCTGCCCATGCCCACT 425

## RESULT 6

AL540575

LOCUS

DEFINITION AL540575 LTL1\_FLO02\_PL1 Homo sapiens cDNA clone CS0DE002YE07 5 prime  
mRNA sequence.

ACCESSION AL540575

VERSION

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 924)

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

Location/Qualifiers

1..924

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DE002YE07"

/clone\_lib="LTL1\_FLO02\_PL1"

/lab\_host="DH10B"

/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand

cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-stranded cDNA was digested with Not I

and cloned into the Not I and Eco RV sites of the

PCMVSPORT 6 vector. Library was constructed by Life

Technologies. Contact : Feng Liang Life Technologies, a

division of Invitrogen 9800 Medical Center Drive Rockville

, Maryland 20850, USA Fax : (1) 301 610 8371 Email :

[fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com>

BASE COUNT 153 a 307 c 299 g 165 t

ORIGIN

Query Match 100.0%; Score 34; DB 9; Length 924;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGAACCGGCTGCCCATGCCCACT 34  
|||||  
DB 838 AGGCTCCGGAGAACCGGCTGCCCATGCCCACT 871

## RESULT 7

AI220927/c

LOCUS

DEFINITION AI220927 599 bp mRNA linear EST 29-NOV-1998  
qg08a11.x1 Soares\_placenta\_8to9weeks\_2NDHP8to9W Homo sapiens cDNA

clone IMAGE:1758908 3' similar to gb:M13981 INHIBIN ALPHA CHAIN  
 PRECURSOR (HUMAN);, mRNA sequence.  
 AI220927  
 AI220927.1 GI:3803130  
 EST.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 599)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Insert Length: 761 Std Error: 0.00  
 Seq primer: -40up from Gibco  
 High quality sequence stop: 379.  
 Location/Qualifiers  
 1..599  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1758908"  
 /clone\_lib="Soares\_placenta\_8to9weeks\_2NBHP8to9W"  
 /dev\_stage="two placentae: one from 8 weeks and another  
 from 9 weeks post conception"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: placenta; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAAGGAGCGCGCGGATTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M.Fatima Bonaldo."  
 BASE COUNT 135 a 142 c 203 g 115 t 4 others  
 ORIGIN  
 Query Match 95.3%; Score 32.4; DB 9; Length 599;  
 Best Local Similarity 97.1%; Pred. No. 0.16;  
 Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGGCCTCGGAGGACGGCTGCCCATGCCAACT 34  
 |||||  
 DB 540 AGGCCTCGGAGGACGGCTGCCCATGCCAACT 507  
 |||||  
 RESULT 8  
 B0013783/c  
 LOCUS  
 DEFINITION  
 UI-1-BC1p-alb-g-08-0-UI.s1 NCI CGAP P13 Homo sapiens cDNA clone  
 UI-1-BC1p-alb-g-08-0-UI 3', mRNA sequence.  
 ACCESSION  
 B0013783.1  
 VERSION  
 B0013783.1  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 548)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Steven Brown  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.  
 Location/Qualifiers  
 1..548  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="UI-1-BC1p-alb-g-08-0-UI"  
 /clone\_lib="NCI CGAP P13"  
 /tissue\_type="placenta"  
 /dev\_stage="8-9 weeks"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Organ: Placenta; Vector: pT73-Pac (Pharmacia) with  
 a modified polylinker; Site.1: EcoR I; Site.2: Not I;  
 NCI CGAP P13 is a subcloned cDNA library constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are GA, AGGA. For  
 additional information, contact: Bento Soares,  
[bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
 TAG.LIB=UI-1-BC1p  
 TAG.TISSUE=placenta human 8 week  
 TAG\_SEQ=GA  
 BASE COUNT 122 a 123 c 185 g 118 t  
 ORIGIN  
 Query Match 88.2%; Score 30; DB 14; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 CTCGGAGGAGAACGGCTGCCCATGCCAACT 34  
 |||||  
 DB 548 CTCGGAGGAGAACGGCTGCCCATGCCAACT 519  
 |||||  
 RESULT 9  
 A1885743/c  
 LOCUS  
 DEFINITION  
 w61a07.x1 NCI CGAP Bn25 Homo sapiens cDNA clone IMAGE:2429364 3'  
 similar to gb:M13981 INHIBIN ALPHA CHAIN PRECURSOR (HUMAN);, mRNA  
 sequence.  
 ACCESSION  
 A1885743  
 VERSION  
 A1885743.1  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 510)  
 NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BTGP), Tumor Gene Index  
 Unpublished (1998)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/borip/image/image.html](http://www.bio.llnl.gov/borip/image/image.html)



```

QY 1 AGGCTCCGAGGAAACGGCTGCCCATGCCCAACT 34
||||||| ||||| || || ||||| ||||| |||
Db 75 AGGCTCCGAGGAGCGCGCGCCCATGCCGCACT 108

RESULT 12
LOCUS AA234854 466 bp mRNA linear EST 06-AUG-1997
DEFINITION z177901.r1 Soares_NhMMPu_S1 Homo sapiens cDNA clone IMAGE:669456 5'
similar to gb:M13981 INHIBIN ALPHA CHAIN PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION AA234854
VERSION AA234854.1 GI:1859384
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
AUTHORS Hillier,L., Allen,M., Bowles,L., Duboue,T., Geisel,G., Jost,S.,,
Kucaba,I., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
, Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 676 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..466
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:5563423"
/db_xref="taxon:9606"
/clone="IMAGE:669456"
/clone_lib="Soares_NhMMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/Note="Organ: mixed (see below); Vector: pT73D-pac
(pharmacia) with a modified polylinker; Site.1: Not f;
Site.2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NHM, pregnant uterus
NBHPU, and fetal heart NDH19W) were mixed, and ss circles
were used in vitro. Following HAP purification, this DNA
was made as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 79 a 151 c 119 g 116 t 1 others
ORIGIN
Query Match 76.5%; Score 26; DB 9; Length 466;
Best Local Similarity 85.3%; Pred. No. 28;
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGGAAACGGCTGCCCATGCCCAACT 34
||||||| ||||| || || ||||| ||||| |||
Db 62 AGGCTCCGAGAGACGGCTGCCATGCCCAACT 95

RESULT 13
LOCUS BE721322
DEFINITION 188456 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
VERSION BE721322
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 561)
AUTHORS Smith,T.P.L., Grosse,W.M., Breking,B.A., Roberts,A.J., Stone,R.T.,
Casas,R., Wray,G.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Jaegerid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perlea,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and
Keeler,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAACAGCTATCACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 39 row: M column: 6
Seq primer: ATTAGGTGACAGTATAG.
Location/Qualifiers
1..561
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2B0V"
/tissue_type="pooled"
/lab_host="BH10B"
/Note="vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 80 a 224 c 158 g 99 t
ORIGIN
Query Match 76.5%; Score 26; DB 12; Length 561;
Best Local Similarity 85.3%; Pred. No. 29;
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGGAAACGGCTGCCCATGCCCAACT 34
||||||| ||||| || || ||||| ||||| |||
Db 489 AGGCTCCGAGGAGCGCGCGCCCATGCCCACT 522

RESULT 14
LOCUS BM460913 1074 bp mRNA linear EST 05-FEB-2002
DEFINITION ACENCOUHT.6419289 NCL_CGAP_Ov44 Mus musculus cDNA clone
IMAGE:5504258 5', mRNA sequence.
ACCESSION BM460913
VERSION BM460913.1 GI:18509953
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1074)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

```

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: c9dpps-r@mail.nih.gov  
 Tissue Procurement: Aaron Hsueh  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM12145 row: f column: 03  
 High quality sequence start: 16  
 High quality sequence stop: 739.  
 Location/Qualifiers

## FEATURES

source

1. .1074  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5504258"  
 /clone\_lib="NCI-CGAP\_Ov44"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: ovary; PMSG-treated; Vector:  
 PCMV-SPORT6.cdb; Site\_1: EcoRV; Site\_2: NotI; Cloned  
 unidirectionally. Primer: Oligo dT. Average insert size  
 2.2 kb. Library constructed by Life Technologies. Note:  
 this is a NCI-CGAP Library."

BASE COUNT 176 a 343 c 319 g 232 t 4 others

## ORIGIN

Query Match 76.5%; Score 26; DB 13; Length 1074;  
 Best Local Similarity 85.3%; Pred. No. 33;  
 Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGGCCTCCGGAGGAGACCGCTGCCATGCCAACT 34

||||||| ||||||| ||||||| ||||||| ||

DB 815 AGGCCTCCGGAGGAGACCGCTGCCATGCCCTTCT 848

## RESULT 15

BM461343

LOCUS

BM461343 1118 bp mRNA linear EST 05-FEB-2002

AGENCOURT\_6419744 NCI-CGAP\_Ov44 Mus musculus cDNA clone

IMAGE:5504094 5', mRNA sequence.

ACCESSION

BM461343

VERSION

BM461343.1

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1118)

REFERENCE

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: c9dpps-r@mail.nih.gov

Tissue Procurement: Aaron Hsueh

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12144 row: o column: 07

High quality sequence stop: 672.

Location/Qualifiers

1. .1118

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="IMAGE:5504094"

/clone\_lib="NCI-CGAP\_Ov44"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: ovary; PMSG-treated; Vector:  
PCMV-SPORT6.cdb; Site\_1: EcoRV; Site\_2: NotI; Cloned  
unidirectionally. Primer: Oligo dT. Average insert size

2.2 kb. Library constructed by Life Technologies. Note:  
 this is a NCI-CGAP Library."  
 BASE COUNT 179 a 372 c 323 g 244 t

## ORIGIN

Query Match 76.5%; Score 26; DB 13; Length 1118;

Best Local Similarity 85.3%; Pred. No. 33;

Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGGCCTCCGGAGGAGACCGCTGCCATGCCAACT 34

||||||| ||||||| ||||||| ||||||| ||

DB 793 AGGCCTCCGGAGGAGACCGCTGCCATGCCCTTCT 826

Search completed: March 11, 2003, 10:25:57

Job time : 1173.39 secs